

## Supplemental File 1

Usage:

*splicev -b [one or more bam files] -gtf [one gtf file] -g [gene to plot]*

all arguments:

- h, --help** show help message
- b, --bam** Path to bam file(s)
- t, --transcript** Name of transcript to plot (must match "transcript\_id" field of gtf file)
- g, --gene** Name of gene to plot (overrides "-t" flag). Will plot the longest transcript derived from that gene
- gtf** Path to gtf file
- bsj** Path to backsplice junction bed-formatted files (listed in the same order as the input bam files)
- sj** Path to canonical splice junction bed-formatted files (listed in the same order as the input bam files)
- stranded** If strand-specific sequencing, indicate 'forward' if upstream reads are forward strand, otherwise indicate 'reverse' (True-Seq is 'reverse')
- is, --intron-scale** The factor by which intron white space should be reduced
- c, --color** Exon color. Hex colors (i.e. "#4286f4". For hex, an escape "\" must precede the argument), RGB (i.e. 211,19,23) or names (i.e. "red")
- f, --filter** Filter out splice junctions and circles that have fewer than this number of counts
- n, --normalize** Normalize coverage between samples
- rc, --reduce\_canonical** Factor by which to reduce canonical curves
- rbs, --reduce\_backsplice** Factor by which to reduce backsplice curves
- ro, --repress\_open** Do not automatically open plot in browser
- en, --exon\_numbering** Label exons

**-rnabp** List of RNA binding proteins to plot.

**-rnabpc** Colors to use for RNABPs

**-fa** Path to fasta file

**-format** Output image format {SVG,PDF,PNG,JPG,TIFF}

**-alu** Path to Alu bed file